

CB



PCT09

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/926,256

TIME: 18:35:09

Input Set : A:\214595US0PCT.ST25.txt

Output Set: N:\CRF3\02062002\I926256.raw

ENTERED

3 <110> APPLICANT: FUKUCHI, NAOYUKI
 4 KAGEYAMA, SHUNSUKE
 5 KITO, MORIKAZU
 6 KAYAHARA, TAKASHI
 7 YAMAMOTO, HIROSHI
 9 <120> TITLE OF INVENTION: Method for Producing Subunit Peptide Originating from
 Oligomeric Protein
 11 <130> FILE REFERENCE: 214595US0PCT
 13 <140> CURRENT APPLICATION NUMBER: US 09/926,256
 14 <141> CURRENT FILING DATE: 2001-10-02
 16 <150> PRIOR APPLICATION NUMBER: JP 11-96073
 17 <151> PRIOR FILING DATE: 1999-04-02
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 126
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Crotalus horridus horridus
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 31 1 5 10 15
 34 Lys Pro Phe Lys Gln Glu Met Thr Trp Ala Asp Ala Gln Arg Phe Cys
 35 20 25 30
 38 Ser Glu Gln Ala Lys Gly Gly His Leu Leu Ser Val Glu Thr Ala Leu
 39 35 40 45
 42 Glu Ala Ser Phe Val Asp Asn Val Leu Tyr Ala Asn Lys Glu Tyr Leu
 43 50 55 60
 46 Thr Arg Tyr Ile Trp Ile Gly Leu Arg Val Gln Asn Lys Gly Gln Pro
 47 65 70 75 80
 50 Cys Ser Ser Ile Ser Tyr Glu Asn Leu Val Asp Pro Phe Glu Cys Phe
 51 85 90 95
 54 Met Val Ser Arg Asp Thr Arg Leu Arg Glu Trp Phe Lys Val Asp Cys
 55 100 105 110
 58 Glu Gln Gln His Ser Phe Ile Cys Lys Phe Thr Arg Pro Arg
 59 115 120 125
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 63 <211> LENGTH: 17
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 67 <220> FEATURE:
 68 <223> OTHER INFORMATION: SYNTHETIC DNA
 70 <220> FEATURE:
 71 <221> NAME/KEY: misc_feature
 72 <222> LOCATION: (12)..(12)

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82 <212> TYPE: DNA
83 <213> ORGANISM: ARTIFICIAL SEQUENCE
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86 <223> OTHER INFORMATION: SYNTHETIC DNA
88 <220> FEATURE:
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90 <222> LOCATION: (3)..(3)
91 <223> OTHER INFORMATION: n=a, g, c or t
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95 tcnacyttra accaytc 17
98 <210> SEQ ID NO: 4
99 <211> LENGTH: 272
100 <212> TYPE: DNA
101 <213> ORGANISM: Crotalus horridus horridus
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104 caggagatga cttgggcccga tgcagagagg ttctgctcgg agcaggcgaa gggcgggcat 60
106 ctcctctctg tcgaaaccgc cctagaagca tcctttgtgg acaatgtgct ctatgcgaac 120
108 aaagagtacc tcacacgtta tatctggatt ggactgaggg ttcaaaacaa aggacagcca 180
110 tgcctccagca tcagttatga gaacctggtt gacccatttg aatgttttat ggtgagcaga 240
112 gacacaaggc ttcgtgagtg gttcaaagtc ga 272
115 <210> SEQ ID NO: 5
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117 <212> TYPE: DNA
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122 <222> LOCATION: (66)..(512)
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127 ctgagcagac ttgctacctg tggaggccga ggaacagttc tctctgcagg gaaggaaaga 60
129 acgcc atg ggg cga ttc atc ttc gtg agc ttc aac ttg ctg gtc gtg ttc 110
130 Met Gly Arg Phe Ile Phe Val Ser Phe Asn Leu Leu Val Val Phe
131 1 5 10 15
133 ctc tcc cta agt gga act cta gct gat ttg gaa tgt ccc tcc ggt tgg 158
134 Leu Ser Leu Ser Gly Thr Leu Ala Asp Leu Glu Cys Pro Ser Gly Trp
135 20 25 30
137 tct tcc tat gat cgg tat tgc tac aag ccc ttc aaa caa gag atg acc 206
138 Ser Ser Tyr Asp Arg Tyr Cys Tyr Lys Pro Phe Lys Gln Glu Met Thr
139 35 40 45
141 tgg gcc gat gca gag agg ttc tgc tcg gag cag gcg aag ggc ggg cat 254
142 Trp Ala Asp Ala Glu Arg Phe Cys Ser Glu Gln Ala Lys Gly Gly His
143 50 55 60
145 ctc ctc tct gtc gaa acc gcc cta gaa gca tcc ttt gtg gac aat gtg 302
146 Leu Leu Ser Val Glu Thr Ala Leu Glu Ala Ser Phe Val Asp Asn Val

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147      65      70      75
149 ctc tat gcg aac aaa gag tac ctc aca cgt tat atc tgg att gga ctg      350
150 Leu Tyr Ala Asn Lys Glu Tyr Leu Thr Arg Tyr Ile Trp Ile Gly Leu
151 80      85      90      95
153 agg gtt caa aac aaa gga cag cca tgc tcc agc atc agt tat gag aac      398
154 Arg Val Gln Asn Lys Gly Gln Pro Cys Ser Ser Ile Ser Tyr Glu Asn
155      100      105      110
157 ctg gtt gac cca ttt gaa tgt ttt atg gtg agc aga gac aca agg ctt      446
158 Leu Val Asp Pro Phe Glu Cys Phe Met Val Ser Arg Asp Thr Arg Leu
159      115      120      125
161 cgt gag tgg ttt aaa gtt gac tgt gaa caa caa cat tct ttc ata tgc      494
162 Arg Glu Trp Phe Lys Val Asp Cys Glu Gln Gln His Ser Phe Ile Cys
163      130      135      140
165 aag ttc acg cga cca cgt taagatccgg ctgtgtgaag tctggagaag      542
166 Lys Phe Thr Arg Pro Arg
167      145
169 caaggaagcc cccacacct cccacacccc caccctccgc aatctctgct cttccccctt      602
171 tgctcagtg atgctctctg tagccggatc tgggttttct gctccagatg ggtcagaaga      662
173 tccaataaat tctgcctacc caaaaaaa      690
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178 <212> TYPE: PRT
179 <213> ORGANISM: Crotalus horridus horridus
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184 1      5      10      15
187 Ser Leu Ser Gly Thr Leu Ala Asp Leu Glu Cys Pro Ser Gly Trp Ser
188      20      25      30
191 Ser Tyr Asp Arg Tyr Cys Tyr Lys Pro Phe Lys Gln Glu Met Thr Trp
192      35      40      45
195 Ala Asp Ala Glu Arg Phe Cys Ser Glu Gln Ala Lys Gly Gly His Leu
196      50      55      60
199 Leu Ser Val Glu Thr Ala Leu Glu Ala Ser Phe Val Asp Asn Val Leu
200 65      70      75      80
203 Tyr Ala Asn Lys Glu Tyr Leu Thr Arg Tyr Ile Trp Ile Gly Leu Arg
204      85      90      95
207 Val Gln Asn Lys Gly Gln Pro Cys Ser Ser Ile Ser Tyr Glu Asn Leu
208      100      105      110
211 Val Asp Pro Phe Glu Cys Phe Met Val Ser Arg Asp Thr Arg Leu Arg
212      115      120      125
215 Glu Trp Phe Lys Val Asp Cys Glu Gln Gln His Ser Phe Ile Cys Lys
216      130      135      140
219 Phe Thr Arg Pro Arg
220 145
223 <210> SEQ ID NO: 7
224 <211> LENGTH: 30
225 <212> TYPE: DNA
226 <213> ORGANISM: ARTIFICIAL SEQUENCE
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236 <211> LENGTH: 30
237 <212> TYPE: DNA
238 <213> ORGANISM: ARTIFICIAL SEQUENCE
240 <220> FEATURE:
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244 aataagctta acgtggtcgc gtgaacttgc 30
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248 <211> LENGTH: 26
249 <212> TYPE: DNA
250 <213> ORGANISM: ARTIFICIAL SEQUENCE
252 <220> FEATURE:
253 <223> OTHER INFORMATION: SYNTHETIC DNA
255 <400> SEQUENCE: 9
256 gatgctggag gctggctgtc ctttgt 26
259 <210> SEQ ID NO: 10
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261 <212> TYPE: DNA
262 <213> ORGANISM: ARTIFICIAL SEQUENCE
264 <220> FEATURE:
265 <223> OTHER INFORMATION: SYNTHETIC DNA
267 <400> SEQUENCE: 10
268 ggacagccag cctccagcat cagtta 26

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VERIFICATION SUMMARY

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L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3